

STIC Biotechnology Systems Branch
RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/589,955
Source: 1FWP
Date Processed by STIC: 8/28/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221**

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. **EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE**
2. **U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450**
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314**

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED**SUGGESTED CORRECTION****SERIAL NUMBER: 10/589,955**

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 Wrapped Nucleic
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 Skipped Sequences
 (OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 Skipped Sequences
 (NEW RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

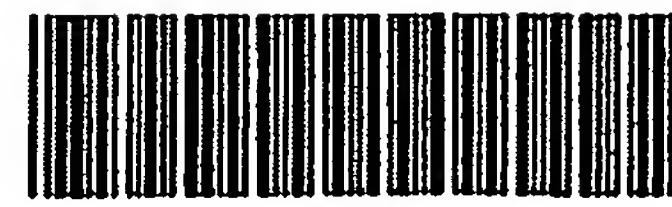
9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

11 Use of <220>
 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWD

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/589,955

DATE: 08/28/2006
TIME: 09:40:09

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\08282006\J589955.raw

3 <110> APPLICANT: National Institute of Advanced Industrial Science and Technology
4 Kinki University
5 Kitakyushu Foundation for the Advancement of Industry
7 <120> TITLE OF INVENTION: Cytoplasm-localized DNA and RNA
9 <130> FILE REFERENCE: 05-102NIQ
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/589,955
C--> 11 <141> CURRENT FILING DATE: 2006-08-18
11 <150> PRIOR APPLICATION NUMBER: JP 2004-045488
12 <151> PRIOR FILING DATE: 2004-02-20
14 <150> PRIOR APPLICATION NUMBER: JP 2004-136228
15 <151> PRIOR FILING DATE: 2004-04-30
17 <160> NUMBER OF SEQ ID NOS: 28
19 <170> SOFTWARE: PatentIn version 3.1

Section 4 on
Error summary
sheet
Does Not Comply
Corrected Diskette Needed

All pp 1-6

ERRORED SEQUENCES

133 <210> SEQ ID NO: 9
134 <211> LENGTH: 21
135 <212> TYPE: RNA
136 <213> ORGANISM: Artificial
138 <220> FEATURE:
139 <223> OTHER INFORMATION: Probe
141 <400> SEQUENCE: 9
E--> 142 cuacaucaacg ccagucaact t
145 <210> SEQ ID NO: 10
146 <211> LENGTH: 21
147 <212> TYPE: RNA
148 <213> ORGANISM: Artificial
150 <220> FEATURE:
151 <223> OTHER INFORMATION: Probe
153 <400> SEQUENCE: 10
E--> 154 guugacuggc gugauguact t
259 <210> SEQ ID NO: 19
260 <211> LENGTH: 22
261 <212> TYPE: RNA
262 <213> ORGANISM: Artificial
264 <220> FEATURE:
265 <223> OTHER INFORMATION: Linker
267 <220> FEATURE:
268 <221> NAME/KEY: modified_base
269 <222> LOCATION: (1)..(1)
270 <223> OTHER INFORMATION: Linker

It's not allowed in an RNA sequence.
For a combined DNA/RNA sequence,
use <2127 DNA and replace in
2207-2237
21 section

same error

21

same

RAW SEQUENCE LISTING
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Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\08282006\J589955.raw

273 <220> FEATURE:
274 <221> NAME/KEY: misc_feature
275 <222> LOCATION: (1)..(1)
276 <223> OTHER INFORMATION: "n" is -O-CH.sub.2CH.sub.2-O-CH.sub.2CH.sub.2-NH.sub.2
279 <400> SEQUENCE: 19
E--> 280 ncuacaucac gccagucAAC tt 22

"n" can only represent
a single nucleotide, nothing
else

283 <210> SEQ ID NO: 20
284 <211> LENGTH: 22
285 <212> TYPE: RNA
286 <213> ORGANISM: Artificial
288 <220> FEATURE:
289 <223> OTHER INFORMATION: Linker
291 <220> FEATURE:
292 <221> NAME/KEY: modified_base
293 <222> LOCATION: (1)..(1)
294 <223> OTHER INFORMATION: Linker
297 <220> FEATURE:
298 <221> NAME/KEY: misc_feature
299 <222> LOCATION: (1)..(1)
300 <223> OTHER INFORMATION: "n" is -O-CH.sub.2CH.sub.2-O-CH.sub.2CH.sub.2-NH.sub.2

same error as above

303 <400> SEQUENCE: 20
E--> 304 nguugacugg cgugauuguAG tt 22
307 <210> SEQ ID NO: 21
308 <211> LENGTH: 21
309 <212> TYPE: RNA
310 <213> ORGANISM: Artificial
312 <220> FEATURE:
313 <223> OTHER INFORMATION: Modified thymidine
315 <220> FEATURE:
316 <221> NAME/KEY: modified_base
317 <222> LOCATION: (20)..(20)
318 <223> OTHER INFORMATION: Modified thymidine

This does not describe Artificial
Sequence

) not acceptable in an RNA
sequence

321 <400> SEQUENCE: 21
E--> 322 cuacaucacg ccagucaact t 21
325 <210> SEQ ID NO: 22
326 <211> LENGTH: 21
327 <212> TYPE: RNA
328 <213> ORGANISM: Artificial
330 <220> FEATURE:
331 <223> OTHER INFORMATION: Modified thymidine
333 <220> FEATURE:
334 <221> NAME/KEY: modified_base
335 <222> LOCATION: (20)..(20)
336 <223> OTHER INFORMATION: Modified thymidine

same error as above

same

339 <400> SEQUENCE: 22
E--> 340 guugacuggc gugauuguAG t 21
343 <210> SEQ ID NO: 23
344 <211> LENGTH: 21
345 <212> TYPE: RNA

21

RAW SEQUENCE LISTING
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TIME: 09:40:09

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\08282006\J589955.raw

346 <213> ORGANISM: Artificial
348 <220> FEATURE:
349 <223> OTHER INFORMATION: Modified thymidine *dmn*
351 <220> FEATURE:
352 <221> NAME/KEY: modified_base
353 <222> LOCATION: (6)..(6)
354 <223> OTHER INFORMATION: Modified thymidine
357 <220> FEATURE:
358 <221> NAME/KEY: modified_base
359 <222> LOCATION: (15)..(15)
360 <223> OTHER INFORMATION: Modified thymidine

363 <400> SEQUENCE: 23
E--> 364 cuacaucacg ccagucuaact t 21

367 <210> SEQ ID NO: 24
368 <211> LENGTH: 21
369 <212> TYPE: RNA
370 <213> ORGANISM: Artificial
372 <220> FEATURE:
373 <223> OTHER INFORMATION: Modified thymidine
375 <220> FEATURE:
376 <221> NAME/KEY: modified_base
377 <222> LOCATION: (7)..(7)
378 <223> OTHER INFORMATION: Modified thymidine
381 <220> FEATURE:
382 <221> NAME/KEY: modified_base
383 <222> LOCATION: (12)..(12)
384 <223> OTHER INFORMATION: Modified thymidine
387 <220> FEATURE:
388 <221> NAME/KEY: modified_base
389 <222> LOCATION: (15)..(15)
390 <223> OTHER INFORMATION: Modified thymidine
393 <220> FEATURE:
394 <221> NAME/KEY: modified_base
395 <222> LOCATION: (17)..(17)
396 <223> OTHER INFORMATION: Modified thymidine

399 <400> SEQUENCE: 24
E--> 400 guugacuggc gugauguagt t 21

403 <210> SEQ ID NO: 25
404 <211> LENGTH: 23
405 <212> TYPE: RNA
406 <213> ORGANISM: Artificial
408 <220> FEATURE:
409 <223> OTHER INFORMATION: Linker
411 <220> FEATURE:
412 <221> NAME/KEY: modified_base
413 <222> LOCATION: (1)..(1)
414 <223> OTHER INFORMATION: Linker
417 <220> FEATURE:
418 <221> NAME/KEY: misc_feature

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/589,955

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TIME: 09:40:09

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\08282006\J589955.raw

error

419 <222> LOCATION: (1)..(1)
420 <223> OTHER INFORMATION: "n" is -O-CH.sub.2CH.sub.2-O-CH.sub.2CH.sub.2-NH-R.sup.1
423 <400> SEQUENCE: 25
E--> 424 ncuacauacac gccagucAAC tt 22
427 <210> SEQ ID NO: 26
428 <211> LENGTH: 26
429 <212> TYPE: RNA
430 <213> ORGANISM: Artificial
432 <220> FEATURE:
433 <223> OTHER INFORMATION: Modified thymidine
435 <220> FEATURE:
436 <221> NAME/KEY: modified_base
437 <222> LOCATION: (20)..(20) error
438 <223> OTHER INFORMATION: Modified thymidine
441 <400> SEQUENCE: 26
E--> 442 cuacauacacg ccagucAACT t 21
445 <210> SEQ ID NO: 27
446 <211> LENGTH: 27
447 <212> TYPE: RNA
448 <213> ORGANISM: Artificial
450 <220> FEATURE:
451 <223> OTHER INFORMATION: Modified thymidine
453 <220> FEATURE:
454 <221> NAME/KEY: modified_base
455 <222> LOCATION: (1)..(1)
456 <223> OTHER INFORMATION: Linker
459 <220> FEATURE:
460 <221> NAME/KEY: modified_base
461 <222> LOCATION: (21)..(21) error
462 <223> OTHER INFORMATION: Modified thymidine
465 <220> FEATURE:
466 <221> NAME/KEY: misc_feature
467 <222> LOCATION: (1)..(1)
468 <223> OTHER INFORMATION: "n" is -O-CH.sub.2CH.sub.2-O-CH.sub.2CH.sub.2-NH-R.sup.1
471 <400> SEQUENCE: 27
E--> 472 ncuacauacac gccagucAACT tt 22
475 <210> SEQ ID NO: 28
476 <211> LENGTH: 28
477 <212> TYPE: RNA
478 <213> ORGANISM: Artificial
480 <220> FEATURE:
481 <223> OTHER INFORMATION: Modified thymidine
483 <220> FEATURE:
484 <221> NAME/KEY: modified_base
485 <222> LOCATION: (1)..(1)
486 <223> OTHER INFORMATION: Linker
489 <220> FEATURE:
490 <221> NAME/KEY: modified_base
491 <222> LOCATION: (3)..(3)

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/589,955

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TIME: 09:40:09

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\08282006\J589955.raw

492 <223> OTHER INFORMATION: Modified thymidine
495 <220> FEATURE:
496 <221> NAME/KEY: modified_base
497 <222> LOCATION: (7)..(7)
498 <223> OTHER INFORMATION: Modified thymidine
501 <220> FEATURE:
502 <221> NAME/KEY: modified_base
503 <222> LOCATION: (16)..(16)
504 <223> OTHER INFORMATION: Modified thymidine
507 <220> FEATURE:
508 <221> NAME/KEY: modified_base *err*
509 <222> LOCATION: (21)..(21)
510 <223> OTHER INFORMATION: *Modified thymidine*
513 <220> FEATURE:
514 <221> NAME/KEY: misc_feature
515 <222> LOCATION: (1)..(1)
516 <223> OTHER INFORMATION: "n" is -O-CH₂-CH₂-O-CH₂-CH₂-NH-R¹
519 <400> SEQUENCE: 28
E--> 520 ncuacaucac gccagucaac *tt* *err* *err* 22

O

10/589,955

6

<210> 2
<211> 10
<212> PRT
<213> PKIfi
<400> 2

1) do not use scientific symbols. They cannot be
processed by
2) invalid (213) response
(see item 10 on Error
summary sheet)

Leu Ala Leu Lys Leu Ala Gly Leu Asp Ile

1

5

10

<210> 3
<211> 13
<212> PRT
<213> MAPKK

same error

9 This type of error appears in
subsequent
sequences,
too.

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/589,955

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TIME: 09:40:10

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\08282006\J589955.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:142 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:2
L:154 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:2
L:280 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0
L:280 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:2
L:304 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0
L:304 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:2
L:322 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:2
L:340 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:2
L:364 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:2
L:400 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:2
L:424 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:0
L:424 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:2
L:442 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:2
L:472 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:0
L:472 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:2
L:520 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:0
L:520 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:2